

OM of: US-08-911-423-2 to: N_Geneseq_34.* out_format : pfs

Date: Aug 5, 1999 2:43 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US08911423/runat_05081999_084745_1154/app_query.fasta.1
-DB=N_Geneseq_34 -Qfmt=fastap -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAEXT=7.000 -YGAPOP=10.000 -YGAEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -STAT=1 -MATRIX=pam150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08911423
-NCPU=6 -ICPU=3 -WAIT -THREADS=1

Search information block:

Query: US-08-911-423-2
Query length: 228
Database: N_Geneseq_34.*
Database sequences: 240622
Database length: 94065609
Search time (sec): 110.750000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
N_Geneseq_34.V32773	+ 1195.00	2631.41	4.4e-139	1020	! Mouse glucocorticoid induced TNFR related polypeptide - used
N_Geneseq_34.V19152	+ 1195.00	2630.87	4.7e-139	1073	! Nucleotide sequence of the mouse
N_Geneseq_34.V32774	+ 1161.50	2556.76	6.3e-135	1031	! Mouse GTR-B cDNA. New isolate
N_Geneseq_34.V32775	+ 1155.00	2541.73	4.4e-134	1087	! Mouse GTR-C cDNA. New isolate
N_Geneseq_34.V19153	+ 660.50	1442.32	7.5e-73	1006	! Nucleotide sequence of the human
N_Geneseq_34.V19154	+ 509.50	1109.90	2.8e-54	723	! Truncated human 31222 protein
N_Geneseq_34.V08126	+ 176.00	366.29	6.5e-13	838	! H4-1BB receptor protein cDNA. N
N_Geneseq_34.V07424	+ 176.00	360.66	1.3e-12	1415	! Human 4-1BB polypeptide coding
N_Geneseq_34.V191026	+ 176.00	360.66	1.3e-12	1415	! Human 4-1BB receptor cDNA clone
N_Geneseq_34.V08969	+ 174.00	360.53	1.4e-12	946	! DNA encoding a human h4-1BBSV
N_Geneseq_34.V39546	+ 157.00	324.01	1.5e-10	838	! Human receptor H4-1BB cDNA. Mon
N_Geneseq_34.V092086	+ 158.00	320.43	2.3e-10	1439	! Human receptor induced by lymph
N_Geneseq_34.V07428	+ 153.50	317.16	3.5e-10	768	! Murine 4-1BB polypeptide coding
N_Geneseq_34.V39541	+ 153.50	317.16	3.5e-10	768	! Murine 4-1BB receptor cDNA clone
N_Geneseq_34.V086127	+ 153.50	305.16	1.6e-09	2347	! Mouse receptor 4-1BB cDNA. Mon
N_Geneseq_34.V086127	+ 153.50	305.15	1.7e-09	2350	! 4-1BB receptor protein cDNA. N
N_Geneseq_34.V00826	+ 113.50	230.50	2.4e-05	618	! Mouse type-II membrane polypep
N_Geneseq_34.V00829	+ 113.50	230.50	2.4e-05	618	! Mouse OX40 extracellular domain
N_Geneseq_34.V32636	+ 117.00	230.16	2.5e-05	1317	! Plasmid pDC406/OX40/Fc* encodi
N_Geneseq_34.V41379	+ 115.50	223.01	6.2e-05	1878	! Murine NF-kB receptor activat
N_Geneseq_34.V41373	+ 115.50	223.01	6.2e-05	1878	! Murine NF-kB receptor activat
N_Geneseq_34.V41375	+ 109.00	211.77	0.0003	1391	! RANK partial polypeptide encod
N_Geneseq_34.V41369	+ 109.00	211.77	0.0003	1391	! RANK partial polypeptide encod
N_Geneseq_34.V088758	+ 105.00	205.82	0.0006	1057	! ACT-4 cell surface receptor ch
N_Geneseq_34.V04048	+ 105.00	205.82	0.0006	1057	! ACT-4 h-1 receptor cDNA sequen
N_Geneseq_34.V41376	+ 109.00	203.04	0.0008	3136	! NF-kB receptor activator RANK
N_Geneseq_34.V41370	+ 109.00	203.04	0.0008	3136	! NF-kB receptor activator RANK
N_Geneseq_34.V093257	+ 101.00	199.47	0.0013	834	! Human OX-40 cDNA. Nucleic acid
N_Geneseq_34.V33166	+ 102.00	198.88	0.0014	1083	! Mutated OCIF, OCIF-DCR1, codin
N_Geneseq_34.V33174	+ 100.50	198.55	0.0014	819	! Mutated OCIF, OCIF-CDD2, codin
N_Geneseq_34.V62467	+ 105.00	197.66	0.0016	2781	! Human dendritic cell receptor
N_Geneseq_34.V33179	+ 100.50	196.78	0.0018	966	! Mutated OCIF, OCIF-CSph, codin
N_Geneseq_34.V33171	+ 100.50	196.58	0.0018	984	! Mutated OCIF, OCIF-DDD2, codin
N_Geneseq_34.V33173	+ 100.50	195.82	0.0020	1056	! Mutated OCIF, OCIF-CC, codin
N_Geneseq_34.V33475	+ 100.50	194.69	0.0023	1173	! Human tumour necrosis factor
N_Geneseq_34.V33178	+ 100.50	194.61	0.0024	1182	! Mutated OCIF, OCIF-CBst, codin
N_Geneseq_34.V24487	+ 100.50	194.55	0.0024	1188	! Modified TR1 receptor coding s
N_Geneseq_34.V33172	+ 100.50	194.45	0.0024	1200	! Mutated OCIF, OCIF-CL, codin
N_Geneseq_34.V33163	+ 100.50	194.39	0.0024	1206	! Mutated OCIF, OCIF-C21S, codin
N_Geneseq_34.V33164	+ 100.50	194.39	0.0024	1206	! Mutated OCIF, OCIF-C22S, codin
N_Geneseq_34.V33165	+ 100.50	194.39	0.0024	1206	! Mutated OCIF, OCIF-C23S, codin

N_Geneseq_34.V326685 + 100.50 194.39 0.0024 1206 ! Osteoclastogenesis inhibito
N_Geneseq_34.V20768 + 100.50 194.39 0.0024 1206 ! Human OCIF genome cDNA. Inh
N_Geneseq_34.V96063 + 100.50 193.14 0.0029 1355 ! Human osteoprotegerin cDNA.

seq_name: N_Geneseq_34.V32773

seq_documentation_block:

ID V32773 standard; cDNA; 1020 BP.

AC V32773; 1998 (first entry)

DE Mouse glucocorticoid induced TNFR-family related protein cDNA.

KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;

KW GTR; tumour necrosis factor; apoptosis; hodgkin's disease; GTR-B;

KW GTR-C; ds.

OS Mus sp.

FT Key Location/Qualifiers

FT CDS 46..732

FT sig_peptide 46..102

FT sig_peptide 46..102

FT sig_peptide 46..102

FT sig_peptide 46..102

FT sig_peptide 46..102

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FT sig_peptide 46..102

FT sig_peptide 46..102

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FT sig_peptide 46..102

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67 rHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGlnP 84
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246 CCACGTGTGGAGACCTCAGTCAAGATCTGCAAGCACCTACCCCTGCCAAC 295
84 rOGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
|||||
296 CAGGCCAGAGGCTGAGTCTCAAGGGGATATTGTTTGGCTTCGGGT 345
101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysAr 117
|||||
346 GTTGCCTGTGCATGGGACCTCTCCCGAGGTGCTGACGGTCACTGGCAG 395
117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
|||||
396 ACTTTGGACCAACTGTTCTCAGTTTGGATTCTCACCATTGTTCCCTGGGA 445
134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
|||||
446 ACAAGACCCACAATGCTGTGTGATCCCGGAGCCACTGCCCACTGAGCAA 495
151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
|||||
496 TACGCCCAATTTGACTGTCTCAGTTTGGATTCTCACCATTGTTCCCTGGGA 545
167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
|||||
546 CCTAACCACTGCTGAGTCTGCGCTGCACATATGGCAGCTGAGGAGGCAAC 595
184 isMetCysProArgGluThrGlnPropheAlaGluValGlnLeuSerAla 200
|||||
596 ACATGTGTCTCGAGAGACCCAGCCATTCGCGGAGGTGCAGTTGTCAAGT 645
201 GluAspAlaCysSerPheGlnPheProGluGluGluArgGlyGluGlnTh 217
|||||
646 GAGGATGCTTCAGCTTCCAGTTCCCTCAGGAGGAACGCGGGGAGCAGAC 695
217 rGluGluLysCysHisLeuGlyGlyArgTyrPro 228
|||||
696 AGAGAAAGTGTATCTGGGGGTCTGGTGGCCA 729

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seq_name: N_Geneseq_34:V19152

seq_documentation_block:

ID V19152 standard; DNA; 1073 BP.

AC V19152;

28-JUL-1998 (first entry)

Nucleotide sequence of the mouse 312C2 T cell gene.

Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell;

antigen-specific T cell proliferation; cytokine production by T-cell;

apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;

autoimmune disorders.

OS Mus sp.

Location/Qualifiers

Key 67..754

CDS /*tag= a

/product= "mouse 312C2 protein"

PN W09806842-AL.

PD 19-FEB-1998.

PF 14-AUG-1997; U13931.

PR 07-OCT-1996; US-027901.

PR 16-AUG-1996; US-689943.

PA (SCHE) SCHERING CORP.

PI Gorman DW, Randall TD, Zlotnik A;

DR WPI; 98-159534/14.

DR P-PSDB; W37838.

PT Isolated 312C2 T cell gene - used to develop products for treating,

e.g. cancers, auto-immune disorders, transplantation rejection and

other T cell disorders

PS Claim 10; Pages 56-57; 71pp; English.

CC This is the nucleotide sequence encoding the mouse 312C2 T cell

protein. The 312C2 proteins are expressed in thymus cells and are

induced on T cells and spleen cells following activation. Engagement

CC of 312C2 stimulates proliferation of T cell clones, antigen-specific
 CC proliferation and cytokine production by T-cells, and potentiates T
 CC cell expansion or apoptosis. The products can be used in the
 CC treatment of conditions associated with abnormal physiology or
 CC development, including abnormal proliferation, e.g. cancerous
 CC conditions or degenerative conditions. They can be used in the
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells
 CC which affect immunological responses, e.g. autoimmune disorders.
 SQ Sequence 1073 BP; 243 A; 283 C; 310 G; 237 T;

alignment_scores:
 Quality: 1195.00 Length: 228
 Ratio: 5.241 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-911-423-2 x V19152 ..

Align seg 1/1 to: V19152 from: 1 to: 1073

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1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
|||||
68 ATGGGGGCATGGGCCATGCTGTATGGAGTCTCGATGCTCTGTGTGTGGA 117
17 pLeuGlyGlnProSerValValGluGluProGlyCysGlyProGlyLysV 34
|||||
118 CTAAGTGTAGCCAGGTAGTTGAGGAGCCTGGCTGTGGCCCTGGCAAG 167
34 alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro 50
|||||
168 TTCAGACGGGAAGTGGCAACACACTCGCTGCTGCAGCCTGTATGCTCCA 217
51 GlyLysGluAspCysProLysGluArgCysIleCysValThrProGluTy 67
|||||
218 GGCAAGGAGGACTGTCCAAAGAAAGGTGCATATGTTCACACCTGAGTA 267
67 rHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGlnP 84
|||||
268 CCACGTGTGGAGACCTCAGTGCAGATCTGCAAGACTACCCCTGCCAAC 317
84 rOGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
|||||
318 CAGGCCAGAGGGTGGAGTCTCAAGGGGATATTGTTTGGCTCCGGTGT 367
101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysAr 117
|||||
368 GTTGCTGTGCCATGGCACCTTCTCCGAGGTGCTGACGGTCACTGCAG 417
117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
|||||
418 ACTTTGGACCAACTGTTCTCAGTTTGGATTCTCACCATTGTTCCCTGGGA 467
134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
|||||
468 ACAAGACCCACAATGCTGTGTCATCCCGAGCCACTGCCCACTGAGCAA 517
151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
|||||
518 TACGGCAATTTGACTGTCTCATCTTCTGGTGCATGGCTGCATGCAATTTCTT 567
167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
|||||
568 CCTAACCACTGCTGAGTCTGGCTGCACATATGGCAGCTGAGGAGGCAAC 617
184 isMetCysProArgGluThrGlnPropheAlaGluValGlnLeuSerAla 200
|||||
618 ACATGTGTCCCCGAGAGACCCAGCCATTCCGGAGGTGCAGTTGTGAGCT 667
201 GluAspAlaCysSerPheGlnPheProGluGluGluArgGlyGluGlnTh 217
|||||
668 GAGGATGCTTGCAGCTTCCAGTTCCCTGAGGAGGAACGCGGGGAGCAGAC 717

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217 rGluGluLysCysHisLeuGlyArgTTPPro 228
 718 AGAAGAAAGTGTCTATCTGGGGTGGTGGCCA 751

seq_name: N_Geneseq_34:V32774

seq_documentation_block:

ID V32774 standard; cDNA; 1031 BP.

AC V32774;

DT 29-SEP-1998 (first entry)

DE Mouse GTR-B cDNA.

KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;

KW GTR; tumour necrosis factor; apoptosis; hodgkin's disease; GTR-B;

OS GTR-C; ds.

OS Mus sp.

FH Key

FT CDS

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246 CCACTGTGGAGACCCCTCAGTGCAGATCTGCAAGCACTACCCCTGCCAAC 295
 84 roGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
 296 CAGCCAGAGGGTGGAGTCTCAAGGGGATATGTGTTGGCTTCGGGTGT 345
 101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysArg 117
 346 GTTGCCGTGTCATGGGACCTTCTCCAGAGTGTGACGGTCACTGTCAG 395
 117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
 396 ACTTTGGACCAACTGTTCTCAGTTTGGATTCTCACCATTGTTCCCTGGGA 445
 134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
 446 ACAAGACCCACATGCTGTGTCATCCCGAGCCACTGCCCACTGAGCAA 495
 151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
 496 TACGCCATTGACTGTCATCTCTGTCATGCTGTCATGTCATGTCATTT 545
 167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
 546 CCTAACCCACAGTCCAGCTCGGCTGCACATATGGCAGCTGAGGAGGCAAC 595
 184 isMetCysProArg.....Glu...ThrGlnProPheAlaGluValG 197
 596 ACATGTGTCCCGAGTTTACTACAGAGACCCAGCCATTCCGGAGGTGC 645
 197 inLeuSerAlaGluAspAlaCysSerPheGlnPheProGluGluGluArg 213
 646 AGTTGTGAGCTGAGGATGCTTCCAGTTCCTGAGGAGGAGGAGGAGC 695
 214 GlyGluGlnThrGluGluLysCysHisLeuGlyArgTTPPro 238
 696 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 740

seq_name: N_Geneseq_34:V32775

seq_documentation_block:

ID V32775 standard; cDNA; 1087 BP.

AC V32775;

DT 29-SEP-1998 (first entry)

DE Mouse GTR-C cDNA.

KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;

KW GTR; tumour necrosis factor; apoptosis; hodgkin's disease; GTR-B;

KW GTR-C; ds.

OS Mus sp.

FH Key

FT CDS

FT CDS

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alignment_scores:

Quality: 1161.50 Length: 232

Ratio: 5.094 Gaps: 2

Percent Similarity: 98.276 Percent Identity: 97.845

alignment_block:

US-08-911-423-2 x V32774

Align seg 1/1 to: V32774 from: 1 to: 1031

1 MetClyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
 46 ATGGGGCATGCGGCGATGCTGTATGGAGTCTCGATGCTGTGTGCTGGA 95
 17 pLeuGlyGlnProSerValValGluGluProGlyCysGlyProGlyLysV 34
 96 CCTAGGTACCGCGAGTGTAGTTGAGGAGCTGCTGTGGCCCTGGCAAG 145
 34 alGlnAsnGlySerGlyAsnThrArgCysCysSerLeuTyrAlaPro 50
 146 TTCAGACGGAAGTGGCAACACACTGCTGCGACCGCTGATGCTCCA 195
 51 GlyLysGluAspCysProLysGluArgCysIleCysValThrProGluTy 67
 196 GCGAAGGAGGAGTGTCCAAAGAAAGGTGATGTCACACCTGAGTA 245
 67 rHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGlnP 84

CC the proteins they encode are also claimed to be useful for suppressing
CC growth of tumour cells over-expressing G1FR or for the treatment of
CC refractory hodgkin's disease.
SQ Sequence 1087 BP; 246 A; 287 C; 310 G; 244 T;

alignment_scores:
Quality: 1155.00 Length: 251
Ratio: 5.088 Gaps: 2
Percent Similarity: 90.438 Percent Identity: 90.438
alignment_block:
US-08-911-423-2 x V32775 ..

Align seg 1/1 to: V32775 from: 1 to: 1087

1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
46 ATGGGGCATGGCCATGCTGTATGAGTCTGATGCTGTGTGCTGGA 95
17 pleuGlyGlnProSerValValGluProGlyCysGlyProGlyLysV 34
96 CCTAGTTCAGCCGAGTGTAGTTGAGGAGCTGGCTGTGCCCTGCAAGG 145
34 alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro 50
146 TTCAGACGGAAGTGGCAACACTGCTGTCGAGCTGTATGCTCCA 195
51 GlyLysGluAspCysProLysGluArgCysIleCysValThrProGluTyr 67
196 GGCAGAGGAGTGTCCAAAGAAAGTGCATATGTCACACCTGAGTA 245
67 rHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGlnP 84
246 CCACGTGTGAGACCTTCAGTCAAGATCTGCAAGCACTACCCCTGCCAAC 295
84 roGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
296 CAGGCGCAGAGGTGGAGTCTCAAGGGGATATTGTTGGCTTCGGGTGT 345
101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysAr 117
346 GTTGCTGTGCATGGGACCTTCCTCCGAGGTCTGAGCGTCACTGAG 395
117 GLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
396 ACTTTGGACCACTGTTCTCAGTTTGGATTCTCACCATTGTTCCCTGGA 445
134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
446 ACAAGACCCACAATGCTGTGTCATCCCGAGGCCACTGCCCACTGAGCAA 495
151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePheP 167
496 TACGGCCATTGACTGTCTCTCTGTCATGGCTGCTGATGCTATTTCT 545
167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
546 CTAACACACAGTCCAGCTCGGCTGCACATATGCGAGCTGAGGAGGCAAC 595
184 isMetCysProArg.....Glu..ThrGlnProPheAlaG 195
596 ACATGTGTCCTCCGAGGTGAGTTGTGTCCAGGGAAGGGGAAAAATGTGTCT 645
189Glu..ThrGlnProPheAlaG 195
646 CAGGCCCCCTCACTTACCCAGCTTTTACTACAGAGACCCAGCATTCGCGG 695
195 luValGlnLeuSerAlaGluAspAlaCysSerPheGlnPheProGluGlu 211
696 AGGTGCAGTTGTACAGTGAAGGATGCTTGCAGCTTCAGTTCCCTCAGGAG 745
212 GluArgGlyGluGlnThrGluLysCysHisLeuGlyArgTrpPr 228

|||||
746 GAACGGGGGAGCAGACAGAGAAAAGTGTATCTGGGGGTCTGGTGCC 795
228 o 228
|
796 A 796

seq_name: N_Geneseq_34.V19153

seq_documentation_block:

ID V19153 standard; DNA; 1006 BP.

AC V19153;

DT 28-JUL-1998 (first entry)

DE Nucleotide sequence of the human 312C2 T cell gene.

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

KW antigen-specific T cell proliferation; cytokine production by T-cell;

KW apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;

KW autoimmune disorders.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..726

FT /*tag= a

FT /product= "human 312C2 protein"

PN WO9806842-A1.

PD 19-FEB-1998.

PF 14-AUG-1997; U13931.

PR 07-OCT-1996; US-027901.

PR 16-AUG-1996; US-689943.

PA (SCHE) SCHERING CORP.

PI Gorman DM, Randall TD, Zlotnik A;

DR WPI; 98-159534/14.

DR P-FSDB; W37839.

PT Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and

PT other T cell disorders

PS Claim 10: Pages 58-59; 71pp; English.

CC This is the nucleotide sequence encoding the human 312C2 T cell

CC protein. The 312C2 proteins are expressed in thymus cells and are

CC induced on T cells and spleen cells following activation. Engagement

CC of 312C2 stimulates proliferation of T cell clones, antigen-specific

CC proliferation and cytokine production by T-cells, and potentiates T

CC cell expansion or apoptosis. The products can be used in the

CC treatment of conditions associated with abnormal physiology or

CC development, including abnormal proliferation, e.g. cancerous

CC conditions or degenerative conditions. They can be used in the

CC regulation or development of haematopoietic cells, e.g. lymphoid cells

CC which affect immunological responses, e.g. autoimmune disorders.

SQ Sequence 1006 BP; 156 A; 331 C; 337 G; 182 T;

alignment_scores:

Quality: 660.50 Length: 235

Ratio: 3.458 Gaps: 3

Percent Similarity: 81.277 Percent Identity: 57.021

alignment_block:

US-08-911-423-2 x V19153 ..

Align seg 1/1 to: V19153 from: 1 to: 1006

1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
19 ATGGGGCGCTTTTCGGGCCCTGTGCGGCCCTGGCGCTGCTGTGCGCGCTCAG 68
17 pleuGlyGlnProSerValValGluProGlyCysGlyProGlyLysV 34
69 CTGGGTACAGCCCC...ACCGGGGTCCCGGGTGGCGCTGGCGGCC 115
34 alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAla... 49
116 TCTGCTTGGGACGGGACGAGCGCGCTGCTGCGGGGTTCACACGAG 165
50ProGlyLysGluAspCysProLysGluArgCy 60

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166 CGCTGCTCCCGGATATCCCGGGGAGGAGTGCTGTCCGAGTGGGACTG 215
60 sileCysValThrProGluTyrHisCysGlyAspProGlnCysLysIleC 77
166 CATGTTGTCAGCTGAATTCCTACCTGCGGAGACCTTGTGCGAGACTT 265
77 yslYsHisTyrProCysGlnProGlyGlnArgValGluSerGlnGlyAsp 93
266 GCCGCGACCACTTGTCCCGGAGGCGGAGGTACACTCCAGGGGAAA 315
94 lleValPheGlyPheArgCysValAlaCysAlaMetGlyThrPheSerAl 110
316 TTCAGTTTGGCTTCAGTGTATCAGCTGTGCTCGGGAGACCTTCTCGG 365
110 aGlyArgAspGlyHisCysArgLeuTyrThrAsnCysSerGlnPheGlyP 127
366 GGGCCACGAGGCGGAGTCAACCTTGGACAGACTGCACCCAGTTCGGGT 415
127 heLeuThrMetPheProGlyAsnLysThrHisAsnAlaValCysIlePro 143
416 TTCACAGTGTCTCCCGGAGACCAACAGCCACAGCTGTGTGCGTCCCA 465
144 GluProLeuProThrGluGlnTyrGlyHisLeuThrValIlePheLeuVa 160
466 GGGTCCCGCGCGAGAGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 515
160 lmetAlaAlaCysIlePhePheLeuThrValGlnLeuGlyLeuHisI 177
516 CGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
177 leTyrGlnLeuArgArgGlnHisMetCysProArgGluThrGlnProPhe 193
566 TCTGCGACTGAGGAGTCAAGTGCATGTGCGCGCCGAGAGACCCAGCTG 615
194 AlaGluValGlnLeuSerAlaGluAspAlaCysSerPheGlnPheProGl 210
616 CTGAGGTGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
210 uGluGluArgGlyGluGln...ThrGluGluLysCysHisLeuGlyGlyA 226
666 GGAAGAGCGGGCGAGCGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
226 rgTTP 227
716 TGTGG 720

```

seq_name: N_Geneseq_34.V19154

documentation_block:

V19154 standard; DNA; 723 BP.

AC V19154;

28-JUL-1998 (first entry)

Truncated human 312C2 protein from clone_A8 nucleotide sequence.

Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

antigen-specific T cell proliferation; cytokine production by T-cell;

apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;

autoimmune disorders.

CS Homo sapiens.

Key Location/Qualifiers

FT CDS

1..723

/*tag= a

/product= "truncated human 312C2 protein from clone_A8"

WO9806842-A1.

19-FEB-1998.

14-AUG-1997; U13931.

07-OCT-1996; US-027901.

16-AUG-1996; US-689943.

(SCHE) SCHERING CORP.

PI Gorman DM, Randall TD, Zlotnik A;

DR WPI; 98-159534/14.

DR P-PSDB; W37840.

Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and
PT other T cell disorders
PS Disclosure: Pages 60-61; 71pp; English.
CC This is the reverse translated nucleotide sequence of the truncated
CC human 312C2 T cell protein from clone_A8. The 312C2 proteins are
CC expressed in thymus cells and are induced on T cells and spleen cells
CC following activation. Engagement of 312C2 stimulates proliferation
CC of T cell clones, antigen-specific proliferation and cytokine
CC production by T-cells, and potentiates T cell expansion or apoptosis.
CC The products can be used in the treatment of conditions associated
CC with abnormal physiology or development, including abnormal
CC proliferation, e.g. cancerous conditions or degenerative conditions.
CC They can be used in the regulation or development of haematopoietic
CC cells, e.g. lymphoid cells which affect immunological responses, e.g.
CC autoimmune disorders.
SQ Sequence 723 BP; 80 A; 92 C; 163 G; 94 T;

alignment_scores:

Quality: 509.50 Length: 236

Ratio: 3.107 Gaps: 5

Percent Similarity: 69.492 Percent Identity: 48.729

alignment_block:

US-08-911-423-2 x V19154

Align seg 1/1 to: V19154 from: 1 to: 723

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1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
|||||
19 ATGGGNGCNTTYMGNCNTYNTGYGNGTNGCNYNTYNTGYGNYTWS 68
17 pLeuGlyGlnProSerValGluGluProGlyCysGlyProGlyLysV 34
|||||
69 NYTNGNCARMGNCN...ACNGGNGGNCNGGNTGYGNGCNGGNGMY 115
34 alGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAla... 49
|||||
116 TNYTNTGNGNACNGNACNGAYGCMGNTGYTGYMGNTGNCAYACNACN 165
50 .....ProGlyLysGluAspCysProLysGluArg... 59
|||||
166 MONTGYTGYMGNGAYTAYCCNGGN...GARGARTGYTGYWSNGARTGGA 212
60 .CysIleCysValThrProGluTyrHisCysGlyAspProGlnCysLysI 76
|||||
213 YTGATGTGYGTCNARCNCNGARTTYCAVTGYGNGAYCCNTGYTYACNA 262
76 leCysLysHisTyrProCysGlnProGlyGlnArgValGluSerGlnGly 92
|||||
263 CNTGYMGNCAYCAVCCNTGYCCNCCNGGNCARGGNGTNCARWSNCARGN 312
93 AspIleValPheGlyPheArgCysValAlaCysAlaMetGlyThrPheSe 109
|||||
313 AARTYWSNTTYGGNTTYCARTGYATGAYTGYGNGNACNTTYWS 362
109 rAlaGlyArgAspGlyHisCysArgLeuTyrThrAsnCysSerGlnPheG 126
|||||
363 NGGNGNCAYGARGGNCAYTYAARCCNTGGACNGAYTYACNCARTTYG 412
126 lypPheLeuThrMetPheProGlyAsnLysThrHisAsnAlaValCysIle 142
|||||
413 GNTTYTYTACNCTNTTYCCNGGNAAYAAACNCAVAYGNCNGTNGTYGN 462
143 ProGluProLeuProThrGluGlnTyrGlyHisLeuThrValIlePheLe 159
|||||
463 CCNGNWSNCCNCCNGCNGARCCNTNGGNTGGTYTACNCTNGTNTYNT 512
159 uValMetAlaAlaCysIlePhePheLeuThrThrValGlnLeuGlyLeuH 176
|||||
513 NGCNGTNGCNGTNGTYNTYNTYNTACNWSNCCNCARYTNGGNYTNC 562
176 lsIleTyrP6lnLeuArgArgGlnHisMetCysProArgGluThrGlnPro 192

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|||||
563 AYATHTGTCARYTNMNSNCARTGYATGTGGCCNMNGARACNCARTYN 612
|||||
193 PheAlaGluValGlnLeuSerAlaGluAspAlaCysSerPheGlnPhePr 209
|||||
613 YTNNTGARGTNCNCNCNCNACNARGAYGNCNMGNWNTGTCARTTYCC 662
|||||
209 oGluGluGluArgGlyGlu...GlnThrGluGluLysCysHisLeuGlyG 225
|||||
663 NGARGARARGMNGNGARGMNGNCGNCGNARGARAARGNMGNTNGNG 712
|||||
225 lyArgTirp 227
:: |||
713 AYTNTGG 720

```

seq_name: N_Geneseq_34:Q86126

```

seq_documentation_block:
Q86126 standard; cDNA; 838 BP.
16-OCT-1995 (first entry)
DE H4-1BB receptor protein cDNA.
KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
OS organ transplantation; cell membrane ligand; ss.
FW Homo sapiens.
FH Key Location/Qualifiers
FT cds 41..808
FT /*tag= a
PN WO9507984-A.
PD 23-MAR-1995.
PF 15-SEP-1994; U10457.
PR 16-SEP-1993; US-122796.
PA (INDV ) UNIV INDIANA FOUND.
PI Kwon BS;
DR WPI; 95-131352/17.
DR P-PSDB; R70977.
PT Novel cDNA encoding human receptor protein H4-1BB - useful to
PT produce the protein which is used to treat autoimmune disease
PT and facilitate organ transplantation
PS Claim 2; Fig.2; 36pp; English.
CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
CC using probes based on the mouse receptor protein 4-1BB gene. The PCR
CC product was used to screen a cDNA library of activated human T-cells.
CC The isolated cDNA (Q86126), deposited as NRRL B21131, encoded the
CC human homolog, H4-1BB (R70977), of 4-1BB.
SQ Sequence 838 BP; 218 A; 191 C; 215 G; 214 T;

```

```

alignment_scores:
Quality: 176.00 Length: 269
Ratio: 1.313 Gaps: 16
Percent Similarity: 49.814 Percent Identity: 26.022

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alignment_block:

US-08-911-423-2 x Q86126 ..

Align seg 1/1 to: Q86126 from: 1 to: 838

```

11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluGluPr 27
|||||
71 ACTCTGTCTGCTCCTCAACTTTGAGAGGACAAAGATCATTCAGGATCC 120
27 o.....
121 TTGTAGTAACCTCCAGCTGGTACATTCGTGTGATAATAACAGGAATCAGA 170
|
28 .....GlyCysGlyProGlyLysValGlnAsnGlySerGlyAsnAsn 41
|||||
171 TTTCAGTCCCTGCTCCTCAAAATAGTTTCTCCAGCGCAGGTGGACAAAGG 220
42 Thr.....ArgCysCysSerLeuTyrAlaProGlyGlyG 53
|||||
221 ACCTGTGACATATGAGGCGAGTGAAGGTGTTTC...AGGACGAGGAA 267

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53 uaspCys.....ProLysGluArgCysIleCysValThrProGluT 67
|||||
268 GAGGTGTTCTCTCCACCAGCAATGCAGATGTGACTGC...ACTCCAGGCT 314
|||||
67 yHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGln 83
|||||
315 TTCACCTGCTGGGGCAGGATGCAGCATGTGTGAACAG...GATTGTAAA 361
|||||
84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCy 100
|||||
362 CAAGGCTCAAGAACTGACAAAAAGGT.....TG 390
|||||
100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysA 117
|||||
391 TAAAGACTGTGCTTTGGGACATTTAAGCATGAGAAACGTCGATCTGTC 440
|||||
117 rgLeuTirpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
|||||
441 GACCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGG 490
|||||
134 AsnLysThrAsnAlaValCys..... 141
|||||
491 AGGAAGGAGGAGGACGTGCTGTGGACCATCTCCAGCTGACCTCTCTCC 540
|||||
142 .....IleProGluProLeuProThrGluGlnTyrGlyHis. 153
|||||
541 GGGAGCATCTCTGTGACCCCGCTGCCCTCGAGAGAGCCAGGACACT 590
|||||
154 .....LeuThrValMetPheLeuValMetAlaAlaCys..... 164
|||||
591 CTCGCGACATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 640
|||||
165 .....IlePhePheLeuThrValGlnLeuGlyLeuHisIleTirpGl 179
|||||
641 TTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 675
|||||
179 nLeuArgArgGlnHisMetCysProArgGlu.....T 190
|||||
676 TGTAAACGG.....GGCAGAAAGAAACCTCTGTATATATCA 713
|||||
190 hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
|||||
714 AACAAACCAATTTATGACACAGTACAAACTACTCAAGAGGAAAGATGGCT 763
|||||
205 SerPheGlnPheProGluGluArgGlyGluGlnThrGluGluLysCy 221
|||||
764 ACTGCGGATTTCCAGAGAGAA.....GAAGGAGGATG 798
|||||
221 shisLeu 223
|||||
799 TGAACGTG 805

```

seq_name: N_Geneseq_34:Q75424

seq_documentation_block:

ID Q75424 standard; cDNA to mRNA; 1415 BP.

```

AC Q75424:
DE Human 4-1BB polypeptide coding sequence.
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 120..887
FT /*tag= a
FT /product= 4-1BB polypeptide.
FT signal_peptide 120..188
FT /*tag= b
FT mat_peptide 189..884
FT /*tag= c
PN WO9426290-A.
PD 24-NOV-1994.

```

[illegible]

Align seg 1/1 to: Q75424 from: 1 to: 1415

seq_documentation_block:
ID T91026 standard; cDNA to mRNA; 1415 BP.
AC T91026;
DT 25-FEB-1998 (first entry)
DE Human 4-1BB receptor cDNA clone hu4-1BB.
DE Human 4-1BB receptor cDNA clone hu4-1BB.
KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte;
KW T cell; proliferation; immunostimulant; ss.

AC	T91026;
AD	25-FEB-1998 (first entry)
DE	Human 4-1BB receptor cDNA clone hu4-1BB.
DE	4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte;
KW	T cell; proliferation; immunostimulant; ss.
KW	Homo sapiens.
OS	
OS	
PH	Key
FT	Location/Qualifiers
FT	120..887
FT	/*tag= a
FT	120..188
FT	/*tag= b
FT	189..884
FT	/*tag= c
PN	US5674704-A.
PN	07-OCT-1997.
PF	07-MAY-1993; 060843.
PR	06-MAY-1994; US-236918.
PR	07-MAY-1993; US-060843.
PA	(IMMV) IMMUNEX CORP.
PA	Alderson MR, Goodwin RG, Smith CA;
WI	WPI: 97-502333/46.
DR	P-PSDB; W26658.
PT	DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
PT	T-cell proliferation in vitro, and as research tools
PS	Example 2; Column 43-46; 32pp; English.
PS	This cDNA clone encodes human 4-1BB (see W26658), a member of the
CC	tumour necrosis factor receptor superfamily that is expressed on
CC	cells that include, but are not limited to, stimulated human
CC	peripheral blood lymphocytes. The clone was isolated from a cDNA
CC	library prepared from human peripheral blood T-lymphocytes that
CC	had been activated with phytohaemagglutinin and phorbol myristate
CC	acetate. A fragment of murine 4-1BB DNA (see T91027) was used
CC	as probe. A novel claimed cytokine, designated 4-1BB ligand
CC	(4-1BB-L) has been identified, cloned and sequenced (see W26657)
CC	that binds to 4-1BB. 4-1BB-L, especially its soluble extracellular
CC	domain, can be used to stimulate T-cell proliferation in vitro, a
CC	research tool and as an affinity ligand for purifying 4-1BB.
CC	Sequence 1415 BP; 385 A; 332 C; 333 G;
CC	3365 T;

alignment_scores:		
Quality:	176.00	Length: 269
Ratio:	1.313	Gaps: 16
Percent Similarity:	49.814	Percent Identity: 26.022

[illegible]

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70 yAspProGlnCysLysIleCysLysHisTyrProCysGlnProGlyGlnA 87
   :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
300 GGGGCGAGGATGCGACATGTGTGAACAG...GATTGTAACAAGGTCACAG 346
   :::: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
87 rgValGluSerGlnGlyAspIleValPheGlyPheArgCysValAlaCys 103
   :::: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
347 AACTGACAAAAAAGGT.....TGTAAGAACTGT 375
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
104 AlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysArgLeuTrpH 120
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
376 TGCTTTGGGACATTTAAGCATCAGAAACGTCGACATCTGTCACCCCTGGAC 425
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
120 rAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyAsnLysThr 137
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
426 AAACGTGTTCTTGGATGGAAGCTGTGCTGTGTAATGGGACGAGGAGA 475
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
137 isAsnAlaValCys..... 141
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
476 GGGACGTGTCTGTGGACCATCTTCAGCGGACCTCTCTCCGGGAGCATCC 525
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
142 ...IleProGluProLeuProThrGlnTyrGlyHis.....Le 154
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
526 TCTGTGACCCCGCCTCTGCGCTGACGTCGACTCGGTGCTTCCTCGTGT 575
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
154 uThrValIlePheLeuValMetAlaAlaCys.....IleP 166
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
576 CATCTCCTCTTCTTGTGCGCTGACGTCGACTCGGTGCTTCCTCGTGT 625
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
166 hePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArg 182
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
626 TCTTCTCTCAG.....CTCCGTTCTCTGTTGTTAAACGG 560
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
183 GlnHisMetCysProArgGlu.....ThrGlnProPh 193
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
661 .....GGCAGAAAGAACTCCTGTATATATTCAAAACCACTT 698
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
193 eAla...GluValGlnLeuSer...AlaGluAspAlaCysSerPheGlnP 208
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
699 TATGACACAGTACAACTACTCAAGAGGAGAGATGGCTGTAGCTGCCGAT 748
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
208 heProGluGluGluArgGlyGluGlnThrGluGluLysCysHisLeu 223
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
749 TTCCAGAGAGAA.....GAAGGAGGATGTGAACGTG 780
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```

seq_name: N_Geneseq_34:T39546

```

seq_documentation_block:
T39546 standard; cDNA to mRNA; 838 BP.
12-DEC-1996 (first entry)
DE Human receptor H4-1BB cDNA.
KW keceptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW immunostimulant; cancer; autoimmune disease; graft rejection;
OS therapy; ss.
OS Homo sapiens.
FH key Location/Qualifiers
FT cds 41..808
FT FT /*tag= a
FT mat_peptide 41..805
FT FT /*tag= b
FN WO9629348-A1.
PD 26-SEP-1996.
PR 22-MAR-1996; U03965.
PR 23-MAR-1995; US-409851.
PA (INDV ) UNIV INDIANA FOUND.
PI Kang C, Kwon BS;
DR WPI; 96-443138/44.
DR P-PSDB; W04174.
PT Monoclonal antibody specific for human receptor protein 4-1BB - used
PT to enhance proliferation and activation of T-cells for treatment of
PT cancer and to inhibit specific ligand binding for treating
PT auto:immune diseases

```

PS Disclosure: Page 36-37; 48pp; English.
 CC A cDNA clone (T39546) codes for novel human receptor protein
 CC H4-1BB (W04174), a protein that has the potential to function as
 CC an accessory signaling molecule during T-cell activation and
 CC proliferation. The cDNA clone was isolated from a lambda gt11
 CC cDNA library of activated human T lymphocytes by screening with a
 CC PCR product obtd. by amplification of lymphocyte cDNA using
 CC primers (see also T39542-45) based on the murine 4-1BB cDNA
 CC (T39541). It can be used to produce recombinant H4-1BB useful
 CC for isolating H4-1BB ligands, for stimulating proliferation of
 CC B-cells expressing H4-1BB ligands, for blocking H4-1BB ligand
 CC binding and for raising anti-H4-1BB monoclonal antibody.
 SQ Sequence 838 BP; 218 A; 192 C; 214 T;

alignment_scores:
 Quality: 157.00 Length: 269
 Ratio: 1.180 Gaps: 16
 Percent Similarity: 49.442 Percent Identity: 25.651
 alignment_block:
 US-08-911-423-2 x T39546 ..
 Align seg 1/1 to: T39546 from: 1 to: 838

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11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluGluPr 27
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
71 ACTCTCTTCTGCTCCTCAACTTTGAGAGGACAAAGATCATTTGCAGGATCC 120
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
27 O..... 27
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
121 TTGTAGTAAGTCCCGAGCTGGTACATCTGTGTATAATAACAGGAATCAGA 170
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
28 .....GlyCysGlyProGlyLysValGlnAsnGlySerGlyAsnAsn 41
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
171 TTTCAGTCCCTGCTCCTCAAAATAGTTTCTCCAGCGCAGGTGGACAAAGG 220
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
42 Thr.....ArgCysCysSerLeuTyrAlaProGlyLysG 53
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
221 ACCTGTGACATATGCAGGCGAGTGTAAAGGTGTTTC...AGGACCAAGAA 267
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
53 uAspCys.....ProLysGluArgCysIleCysValThrProGluT 67
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
268 GGAGTGTCTCTCCACGCAATGCAGATGTGTACTGC...ACTCCAGGGT 314
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
67 yrHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGln 83
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
315 TTCACGTGCTGGGCGGAGATGCAGCATGTGTGAACAG...GATTGTGAAA 361
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCy 100
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
362 CAAGGTCAAGAACTGACAAAAAAGGT.....TG 390
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCys 117
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
391 TAAAGACTGTGCTTTGGGACATTTAACGATCAGAAACGTTGGCATCTGTC 440
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117 rgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
441 GACCCCTGCACAAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGG 490
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
134 AsnLysThrHisAsnAlaValCys..... 141
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
491 ACGAAGGAGAGGAGCGTGTCTGTGGACCATCTCCAGCTGACCTCTCTCC 540
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
142 .....IleProGluProLeuProThrGlnTyrGlyHis. 153
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
541 GGGAGCATCTCTGTGACCCCGCTGCCCTGGAGAGAGAGCCAGGACACT 590
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
154 .....LeuThrValIlePheLeuValMetAlaAlaCys..... 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
591 CTCGCGAGATCATCTCTTTTCTTGTTCGCTGACGTCGACTGCGTTCGTC 640
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165 .....IlePhePheLeuThrThrValGlnLeuGlyLeuHisIleTrpG1 179
      ::::::::::::::::::::
641 TTCTGCTGCTTCTCTCAGG.....CTCGGTTCTCTGT 675
179 nleuArgArgGlnHisMetCysProArgGlu.....T 190
      ::::::::::::::::::::
676 TGTAAACGG.....GGCAGAAAGAACTCCTGTATATATCA 713
190 hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
      ::::::::::::::::::::
714 ACAACCATTTATGACACAGTAACTACTCAAGAGGAAGATGGCTGT 763
205 SerPheGlnPheProGluGluArgGlyGluGlnThrGluGluLysCy 221
      ::::::::::::::::::::
764 AGCTGCCGATTTCAGAAAGAA.....GAAGGAGGATG 798
221 shisLeu 223
      ::::::::::::::::::::
799 TGAACGTG 805

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seq_name: N_Geneseq_34:Q92086

seq_documentation_block:

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ID Q92086 standard; DNA; 1439 BP.
AC Q92086;
DT 21-JAN-1996 (first entry)
DE Human receptor induced by lymphocyte activation (ILA) DNA.
KW ILA; receptor inducible by lymphocyte activation; disease diagnosis;
OS antinflammatory; ss.
KW Homo sapiens.
FT key Location/Qualifiers
   cds 140..904
      /*tag= a
      CA2108401-A.
      PD 28-MAR-1995.
      PF 14-OCT-1993; 108401.
      PR 27-SEP-1993; US-127693.
      PA (REGC ) UNIV CALIFORNIA.
      PI Lotz M, Schwarz H;
      DR WPI; 95-194420/26.
      DP P-PSDB; R74087.
      PT New receptor inducible by lymphocyte activation - used to develop
      prods. for the diagnosis and treatment of inflammatory host defence
      pathology.
      PS Claim 52; page 61; 91pp; English.

```

This DNA may be expressed recombinantly for the production of ILA.
The cDNA was isolated from a library constructed from activated
human T-lymphocyte leukemia virus type-1 transformed human T-
lymphocytes.

SQ Sequence 1439 BP; 393 A; 336 C; 346 G; 364 T;

alignment_scores:
Quality: 158.00 Length: 269
Ratio: 1.188 Gaps: 16
Percent Similarity: 49.442 Percent Identity: 25.279

alignment_block:

US-08-911-423-2 x Q92086 ..

Align seg 1/1 to: Q92086 from: 1 to: 1439

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11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluLupr 27
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170 ACTCTGCTGCTGCTCCTCAACTTTGAGAGGACAAATCATTCGAGGATCC 219
27 o.....
220 TTGTACTAACTGCCAGCTGGTATCTCTGTATAATAACAGGAATCAGA 269
28 .....:GlyCysGlyProGlyLysValGlnAsnGlySerGlyAsnAsn 41
      ::::::::::::::::::::
270 TTTCAGAGTCCTCTCTCCAAATAGTTTCTCCAGCGCAGGTGGACAAAGG 319

```

```

42 Thr.....ArgCysCysSerLeuTyraAlaProGlyLysG1 53
      ::::::::::::::::::::
320 ACCTGTGACATATGGAGGAGTAAAGGTGTTTC...AGGACCAGAA 366
53 uAspCys.....ProLysGluArgCysIleCysValThrProGluF 67
      ::::::::::::::::::::
367 GGAGTGTCTCCTCCACCAGCAATGCAGAGTGTGACTGC...ACTCCAGGT 413
67 yrHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGln 83
      ::::::::::::::::::::
414 TTCAGTGGCTGGGGCAGGATGCAGCATGTGTGAACAG...GATTGTAGA 460
84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCy 100
      ::::::::::::::::::::
461 CAAGGTCAAGAACTGACAAAAAAGGT.....TTG 489
100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysA 117
      ::::::::::::::::::::
490 TAAAGACTGTGCTTTGGGACATTTAACGATCAGAAACGTGGCATCTGTC 539
117 rgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
      ::::::::::::::::::::
540 GACCCTGGACAAACTGTCTTGGATGGAAGTCTGTGCTTGTGAATGG 589
134 AsnLysThrHisAsnAlaValCys..... 141
      ::::::::::::::::::::
590 ACAAGAGAGGAGGCGGTGTGTGGACCATCTCCAGCCGACCTCTCTCC 639
142 .....IleProGluProLeuProThrGluGlnTrpGlyHis. 153
      ::::::::::::::::::::
640 GGGAGCATCTCTGTGACGCCGCTGCCCTCGGAGAGAGCCAGACACT 689
154 .....LeuThrValIlePheLeuValMetAlaAlaCys..... 164
      ::::::::::::::::::::
690 CTCGCGAGATCATCTCTCTTCTTTCGCTGACGTCGACTGCGTGTGCTC 739
165 .....IlePhePheLeuThrThrValGlnLeuGlyLeuHisIleTrpG1 179
      ::::::::::::::::::::
740 TTCCTGCTGTTCTCTCTCAG.....CTCCGTTTCTCTGT 774
179 nLeuArgArgGlnHisMetCysProArgGlu.....T 190
      ::::::::::::::::::::
775 TGTAAACGG.....GGCAGAAAGAACTCCTGTATATATCA 812
190 hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
      ::::::::::::::::::::
813 AACAAACCATTTATGAGACCACTACAAACTACTCAAGAGGAAGATGGCTGT 862
205 SerPheGlnPheProGluGluArgGlyGluGlnThrGluGluLysCy 221
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863 AGCTGCCGATTTCAGAAAGAA.....GAAGGAGGATG 897
221 shisLeu 223
      ::::::::::::::::::::
898 TGAACGTG 904

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seq_name: N_Geneseq_34:Q75428

seq_documentation_block:

ID Q75428 standard; cDNA to mRNA; 768 BP.

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AC Q75428;
DT 08-AUG-1995 (first entry)
DE Murine 4-1BB polypeptide coding sequence.
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
OS Mus musculus.
FT key Location/Qualifiers
   cds 1..768
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      /product= 4-1BB polypeptide.
      FT signal_peptide 1..69
      /*tag= b

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104

550 TTGCAGGTCCTTACCTTGTTCCCTGGCGCTGACATCGGCTTTGCTGCTGGC 599


```

795 AATTCCTCCACATATTC.....AAGCAACCATTTAAGAGACCACT 835
198 LeuSerAla.....GluAspAlaCysSerPheGlnPheProGluGluG1 212
   :|||  ||||| ||||| |||||  :|||  ||||| |||||
836 GGAGCAGCTCAAGAGGAAGATGCTTGTAGCTGCCGATGTCACACAGGAAGA 885
212 uArgGly 214
   |  |||
886 AGAAGGA 892

```